SEQUENCE LISTING

<110> Juridical Foundation, Japanese Foundation For Cancer Research

<120> vector for gene therapy of malignamt melanoma, with use of virus having MSH fused protein.

<130> H11-0241J2

<160> 39

<170> PatentIn Ver. 2. 0

<210> 1
<211> 166
<212> DNA
<213> Artificial Sequence

<220>

<223> DNA coding a part of adenovirus type 5 fiber, AS linker peptide and α -MSH.

<220>

<221> CDS

<222> (3).. (113)

<400> 1

```
gg gaa ttc tcg agt tac act ttt tca tac att gcc caa gaa cca tca          47
   Glu Phe Ser Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu Pro Ser
    1                   5                   10                  15
gcc tcc gca tct gct tcc gcc cct gga tcc tac tcc atg gag cac ttc         95
Ala Ser Ala Ser Ala Ser Ala Pro Gly Ser Tyr Ser Met Glu His Phe
                    20                  25                  30
cgc tgg ggc aag ccg gtg taaagaatcg tttgtgttat gtttcaacgt               143
Arg Trp Gly Lys Pro Val
                35
gtttattttt caattgaatt ccc                                             166
```

<210> 2

<211> 126

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 924 used as temprate for PCR amplification of DNA sequence No. 1.

<400> 2

```
cgttgaaaca taacacaaac gattctttac accggcttgc cccagcggaa gtgctccatg      60
gagtaggatc caggggcgga agcagatgcg gaggctgatg gttcttgggc aatgtatgaa     120
aaagtg                                                                126
```

<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 933 used as sense primer for PCR amplification of DNA sequence No. 1.

<400> 3

gggaattctc gagttacact ttttcataca ttgcccaag   39

<210> 4

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 934 used as antisense primer for PCR amplification of DNA sequence No. 1.

<400> 4

gggaattcaa ttgaaaaata aacacgttga aacataacac aaacgattc   49

<210> 5

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1061 used as sense primer for PCR amplification of DNA coding α-MSH and adenovirus fiber poly A signal.

<400> 5

cgggatccta ctccatggag cacttccgct ggggcaagcc ggtgtaagtc gacaagaata   60

aagaatcgtt tgtgtt   76

<210> 6

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1092 used as antisense primer for PCR amplification of DNA coding α-MSH and adenovirus fiber poly A signal.

<400> 6

cggaattcat ggcgccatgt ttaatcagag gt   32

<210> 7

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/asMSHa

<220>

<221> CDS

<222> (1)..(1815)

<400> 7

```
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca    48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
```

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50   55   60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc   240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
    65   70   75   80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac   288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                    85   90   95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta   336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                    100   105   110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
                    115   120   125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130   135   140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   480

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act   528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
          165   170   175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg   576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
              180   185   190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
              195   200   205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act   672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
          210   215   220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act   720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca   768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
              245   250   255

```
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt    816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
        260                 265                 270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag    864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275                 280                 285


ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac    912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
        290                 295                 300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag    960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325                 330                 335


gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
        340                 345                 350


aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1104
```

```
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                 360                 365


tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
        370                 375                 380


agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
   385                 390                 395                 400


ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405                 410                 415


aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420                 425                 430


ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435                 440                 445


tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
        450                 455                 460
```

```
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt    1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465                 470                 475                 480


aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga    1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                    485                 490                 495


ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc    1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
                    500                 505                 510


aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa    1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
                    515                 520                 525


cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac    1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
                    530                 535                 540


aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc    1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                 550                 555                 560


cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca    1728
```

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            565   570   575

tac att gcc caa gaa cca tca gcc tcc gca tct gct tcc gcc cct gga   1776
Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly
            580   585   590

tcc tac tcc atg gag cac ttc cgc tgg ggc aag ccg gtg taa   1818
Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val
            595   600   605

<210> 8

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1037 used as sense primer for PCR amplification of DNA coding human MSH receptor residue 1-154.

<400> 8

gggaattcac catggctgtg cagggatccc agagaagact   40

<210> 9

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1038 used as antisense primer for PCR amplification of DNA coding human MSH receptor residue 150-317.

<400> 9

gggaattcac caggagcatg tcagcacctc ctt   33

<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1039 used as sense primer for PCR amplification of DNA coding human MSH receptor residue 150-317.

<400> 10

ctgcggtacc acagcatcgt gaccctg   27

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1040 used as antisense primer for PCR amplification of DNA coding human MSH receptor residue 1-154.

<400> 11

gctgtggtac cgcagtgcgt agaagat   27

<210> 12

<211> 107

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1075 used as sense primer for PCR amplification of DNA coding β-MSH and adenovirus fiber poly A signal.

<400> 12

cgcggatccg ccgagaagaa ggacgagggc ccctacagga tggagcactt ccgctggggc   60

agcccgccca aggactaagt cgacaagaat aaagaatcgt ttgtgtt   107

<210> 13

<211> 1848

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/asMSHb

<220>

<221> CDS

<222> (1)..(1845)

<400> 13

```
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca    48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
```

                    50   55   60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc   240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65   70   75   80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac   288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                        85   90   95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta   336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                       100   105   110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
                       115   120   125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
                       130   135   140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

```
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act        528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                 170             175


gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg        576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185             190


aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg        624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195                 200             205


gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act        672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
            210                 215             220


ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act        720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca       768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt       816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
```

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag   864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275   280   285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
        290   295   300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
              325   330   335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
              340   345   350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355   360   365

```
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac    1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370               375                 380


agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act    1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385               390                 395                 400


ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag    1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405                 410                 415


aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata    1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
              420                 425                 430


ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata    1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
    435                 440                 445


tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat    1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450                 455                 460


gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt    1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
```

```
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga    1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            485                    490                    495


ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc    1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500                    505                    510


aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa    1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
            515                    520                    525


cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac    1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
            530                    535                    540


aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc    1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                    550                    555                    560


cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca    1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            565                    570                    575
```

```
tac att gcc caa gaa cca tca gcc tcc gca tct gct tcc gcc cct gga     1776
Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly
            580                 585                 590


tcc gcc gag aag aag gac gag ggc ccc tac agg atg gag cac ttc cgc     1824
Ser Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu His Phe Arg
            595                 600                 605


tgg ggc agc ccg ccc aag gac taa                                     1848
Trp Gly Ser Pro Pro Lys Asp
            610                 615
```

<210> 14

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1060 used as antisense primer for PCR amplification
of DNA coding a part of adenovirus type 5 fiber and GS linker peptide.

<400> 14

```
cgggatccag atccagaacc actaccactt ccagaacctt cttgggcaat gtatgaaaaa     60
g                                                                      61
```

<210> 15

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1098 used as antisense primer for PCR amplification of DNA coding a part of adenovirus type 5 fiber and GS linker peptide.

<400> 15

cgtgtggatc cgctgccaga accactacca cttccagaac c   41

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 931 used as sense primer for PCR amplification of DNA coding a part of adenovirus type 5 fiber and GS linker peptide.

<400> 16

ggcctttact tgtttacagc   20

<210> 17

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/gsMSHa

<220>

<221> CDS

<222> (1)..(1815)

<400> 17

```
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca    48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
```

```
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
     50                    55                    60


aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc    240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65                    70                    75                    80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac    288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                    85                    90                    95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta    336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
               100                   105                   110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc    384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
             115                   120                   125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att    432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
     130                   135                   140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa    480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                   150                   155                   160
```

```
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act    528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                 170                 175


gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg    576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190


aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg    624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195                 200                 205


gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act    672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
            210                 215                 220


ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act    720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca    768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245                 250                 255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt    816
```

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
           260   265   270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag   864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
           275   280   285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
           290   295   300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325   330   335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
           340   345   350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
           355   360   365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370   375   380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                 405   410   415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                 420   425   430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
                 435   440   445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
                 450   455   460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   1440

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                485   490   495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
                500   505   510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
                515   520   525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530   535   540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc   1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545   550   555   560

cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca   1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565   570   575

```
tac att gcc caa gaa ggt tct gga agt ggt agt ggt tct ggc agc gga      1776
Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
            580                 585                 590


tcc tac tcc atg gag cac ttc cgc tgg ggc aag ccg gtg taa           1818
Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val
            595                 600                 605
```

<210> 18

<211> 1848

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/gsMSHb

<220>

<221> CDS

<222> (1)..(1845)

<400> 18

```
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca      48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                   10                  15
```

```
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
         20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
         35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
         50                  55                  60


aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc   240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
     65                  70                  75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac   288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                 85                  90                  95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta   336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
         100                 105                 110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   384
```

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
    115   120   125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130   135   140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
    145   150   155   160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act   528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                    165   170   175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg   576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
                    180   185   190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195   200   205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act   672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210   215   220

```
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act     720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca     768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                    245                 250                 255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt     816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
                    260                 265                 270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag     864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
                    275                 280                 285


ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac     912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290                 295                 300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag     960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata    1008
```

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
           325   330   335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
           340   345   350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
           355   360   365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
       370   375   380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
           405   410   415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
           420   425   430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435   440   445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
        450   455   460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            485   490   495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
        500   505   510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
        515   520   525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   1632

```
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530                 535                 540


aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc     1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                 550                 555                 560


cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca     1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565                 570                 575


tac att gcc caa gaa ggt tct gga agt ggt agt ggt tct ggc agc gga     1776
Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
            580                 585                 590


tcc gcc gag aag aag gac gag ggc ccc tac agg atg gag cac ttc cgc     1824
Ser Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu His Phe Arg
        595                 600                 605


tgg ggc agc ccg ccc aag gac taa                                     1848
Trp Gly Ser Pro Pro Lys Asp
    610                 615
```

<210> 19
<211> 128

34/107

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1089 used as sense primer for PCR amplification of DNA coding K21 linker peptide.

<400> 19

ccggaattca gatctggatc taagaagaag aagaagaaaa agaagaaaaa gaagaagaag   60

aaaaaaaaga agaagaaaaa gaaaggatcc taagatatcg tcgacaagaa taaagaatcg   120

tttgtgtt   128

<210> 20

<211> 1893

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/asK21MSHa

<220>

<221> CDS

<222> (1)..(1890)

<400> 20

```
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca      48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc      96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct    144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
                35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc    192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
         50                  55                  60


aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc    240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65                  70                  75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac    288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta    336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
```

```
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                  120                  125
```

```
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
        130                  135                  140
```

```
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                  150                  155                  160
```

```
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act   528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165                  170                  175
```

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg   576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
                180                  185                  190
```

```
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195                  200                  205
```

```
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act    672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210                  215                  220


ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act    720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                  230                  235                  240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca    768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
              245                  250                  255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt    816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
         260                  265                  270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag    864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
         275                  280                  285


ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac    912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
         290                  295                  300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag    960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
```

```
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata    1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325                330                335
```

```
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca    1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340                345                350
```

```
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat    1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
            355                360                365
```

```
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac    1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
         370                375                380
```

```
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act    1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                390                395                400
```

```
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag    1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
            405                410                415
```

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
        420   425   430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435   440   445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
        450   455   460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            485   490   495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500   505   510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

```
    cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac    1632
    Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
        530                 535                 540


    aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc    1680
    Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
    545                 550                 555                 560


    cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca    1728
    His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                    565                 570                 575


    tac att gcc caa gaa cca tca gcc tcc gca tct gct tcc gcc cct gga    1776
    Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly
                580                 585                 590


    tct gga tct aag aag aag aag aag aaa aag aag aaa aag aag aag aag    1824
    Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
        595                 600                 605


    aaa aaa aag aag aag aaa aag aaa gga tcc tac tcc atg gag cac ttc    1872
    Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Tyr Ser Met Glu His Phe
        610                 615                 620
```

cgc tgg ggc aag ccg gtg taa   1893

Arg Trp Gly Lys Pro Val

625   630

<210> 21

<211> 1893

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/gsK21MSHa

<220>

<221> CDS

<222> (1)..(1890)

<400> 21

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca   48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

 1   5   10   15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc   96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

              20   25   30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
         35   40   45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
      50   55   60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc   240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
      65   70   75   80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac   288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
             85   90   95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta   336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
         100   105   110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115   120   125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act   528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                    165   170   175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg   576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
                    180   185   190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
              195   200   205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act   672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
              210   215   220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act   720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

```
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca     768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245                 250                 255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt     816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
              260                 265                 270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag     864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
              275                 280                 285


ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac     912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
              290                 295                 300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag     960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata    1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                  325                 330                 335


gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca    1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
```

```
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                 360                 365
```

```
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
        370                 375                 380
```

```
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                 390                 395                 400
```

```
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405                 410                 415
```

```
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                420                 425                 430
```

```
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435                 440                 445
```

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
   450   455   460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
          485   490   495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
      500   505   510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
    515   520   525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
   530   535   540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc   1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

```
cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca    1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            565                 570                 575
```

```
tac att gcc caa gaa ggt tct gga agt ggt agt ggt tct ggc agc gga    1776
Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
            580                 585                 590
```

```
tct gga tct aag aag aag aag aag aaa aag aag aaa aag aag aag aag    1824
Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
            595                 600                 605
```

```
aaa aaa aag aag aag aaa aag aaa gga tcc tac tcc atg gag cac ttc    1872
Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Tyr Ser Met Glu His Phe
            610                 615                 620
```

```
cgc tgg ggc aag ccg gtg taa                                        1893
Arg Trp Gly Lys Pro Val
625                 630
```

<210> 22

<211> 1923

<212> DNA

<400> 22

```
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca    48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
                35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
        50                  55                  60
```

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc   240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65   70   75   80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac   288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85   90   95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta   336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                100   105   110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115   120   125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130   135   140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act   528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg    576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180             185             190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg    624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195             200             205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act    672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
            210             215             220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act    720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225             230             235             240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca    768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245             250             255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt    816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
        260             265             270
```

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag   864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
    275   280   285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290   295   300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
  305   310   315   320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
        325   330   335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
        340   345   350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355   360   365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            485   490   495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500   505   510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
            515   520   525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
            530   535   540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc   1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545   550   555   560

cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca   1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565   570   575

tac att gcc caa gaa cca tca gcc tcc gca tct gct tcc gcc cct gga   1776

54/107

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly
      580   585   590

tct gga tct aag aag aag aag aag aaa aag aag aaa aag aag aag aag   1824
Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
      595   600   605

aaa aaa aag aag aag aaa aag aaa gga tcc gcc gag aag aag gac gag   1872
Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Ala Glu Lys Lys Asp Glu
      610   615   620

ggc ccc tac agg atg gag cac ttc cgc tgg ggc agc ccg ccc aag gac   1920
Gly Pro Tyr Arg Met Glu His Phe Arg Trp Gly Ser Pro Pro Lys Asp
625   630   635   640

taa   1923

<210> 23

<211> 1923

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/gsK21MSHb

<220>

<221> CDS

<222> (1).. (1920)

<400> 23

```
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca      48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc      96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct     144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc     192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60


aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc     240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac     288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
```

```
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta    336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
        100             105             110
```

```
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc    384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
    115             120             125
```

```
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att    432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130             135             140
```

```
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa    480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145         150             155             160
```

```
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act    528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
        165             170             175
```

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg    576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        180             185             190
```

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
    195   200   205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act   672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210   215   220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act   720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
    225   230   235   240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca   768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245   250   255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt   816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260   265   270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag   864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
    275   280   285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                       325   330   335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                       340   345   350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
                       355   360   365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370   375   380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
            405   410   415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420   425   430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
            435   440   445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
            450   455   460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            485   490   495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

```
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa    1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
     515                    520                    525


cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac    1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
     530                    535                    540


aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc    1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                    550                    555                    560


cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca    1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                    565                    570                    575


tac att gcc caa gaa ggt tct gga agt ggt agt ggt tct ggc agc gga    1776
Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
                    580                    585                    590


tct gga tct aag aag aag aag aag aaa aag aag aaa aag aag aag aag    1824
Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
     595                    600                    605
```

aaa aaa aag aag aag aaa aag aaa gga tcc gcc gag aag aag gac gag   1872
Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Ala Glu Lys Lys Asp Glu
        610   615   620

ggc ccc tac agg atg gag cac ttc cgc tgg ggc agc ccg ccc aag gac   1920
Gly Pro Tyr Arg Met Glu His Phe Arg Trp Gly Ser Pro Pro Lys Asp
625   630   635   640

taa   1923

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding AS linker

<220>

<221> CDS

<222> (1)..(33)

<400> 24

cca tca gcc tcc gca tct gct tcc gcc cct gga   33

Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly

1   5   10

<210> 25

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> AS linker peptide

<400> 25

Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly
1   5   10

<210> 26

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding GS linker

<220>

<221> CDS

<222> (1)..(33)

<400> 26

ggt tct gga agt ggt agt ggt tct ggc agc gga   33

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

1   5   10

<210> 27

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> GS linker peptide

<400> 27

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

1   5   10

<210> 28

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding asK21 linker

<220>

<221> CDS

<222> (1)..(108)

<400> 28

```
cca tca gcc tcc gca tct gct tcc gcc cct gga tct gga tct aag aag    48
Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly Ser Gly Ser Lys Lys
 1               5                  10                  15

aag aag aag aaa aag aag aaa aag aag aag aag aaa aaa aag aag aag    96
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
            20                  25                  30

aaa aag aaa gga                                                   108
Lys Lys Lys Gly
        35
```

<210> 29

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> asK21 linker peptide

<400> 29

Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly Ser Gly Ser Lys Lys
1   5   10   15

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
                20   25   30

Lys Lys Lys Gly
            35

<210> 30
<211> 108
<212> DNA
<213> Artificial Sequence

<220>

<223> DNA coding gsK21 linker

<220>

<221> CDS

<222> (1)..(108)

<400> 30

ggt tct gga agt ggt agt ggt tct ggc agc gga tct gga tct aag aag   48
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Lys Lys
 1   5   10   15

aag aag aag aaa aag aag aaa aag aag aag aag aaa aaa aag aag aag   96
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
            20   25   30

aaa aag aaa gga   108
Lys Lys Lys Gly
         35

<210> 31

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> gsK21 linker peptide

<400> 31

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Lys Lys
 1   5   10   15

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys

Lys Lys Lys Gly
                35

<210> 32

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/asMSHa

<400> 32

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1   5   10   15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20   25   30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
          35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
       50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                    85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                    100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
                    115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
                    130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                    165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
                    180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
                    195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
                260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
                275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

      340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
       355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
     370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
         405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
        420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
    435   440   445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450   455   460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
        485   490   495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
        500   505   510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
        515   520   525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
        530   535   540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
    545   550   555   560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
        565   570   575

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly
        580   585   590

Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val
        595   600.   605

<210> 33

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/asMSHb

<400> 33

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1   5   10   15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20   25   30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
        100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
        130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
                180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
        210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
           245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
           260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
           275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
           290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
           325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
           340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
           355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                     405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                     420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
                     435   440   445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
                     450   455   460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                     485   490   495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
                     500   505   510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515   520   525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530   535   540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545   550   555   560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                    565   570   575

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly
                    580   585   590

Ser Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu His Phe Arg
                    595   600   605

Trp Gly Ser Pro Pro Lys Asp
610   615

<210> 34

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6. 7R-F/gsMSHa

<400> 34

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1   5   10   15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20   25   30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
        50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
        130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
    145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
                180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
        210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
        245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
     260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
    275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
      325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
     340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
     355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
          405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
          420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
          435   440   445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
          450   455   460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
          485   490   495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
          500   505   510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
          515   520   525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530   535   540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
 545   550   555   560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
               565   570   575

Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
           580   585   590

Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val
           595   600   605

<210> 35

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6. 7R-F/gsMSHb

<400> 35

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

```
            1                   5                        10                       15

        Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                    20                      25                      30

        Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
                    35                      40                      45

        Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
                    50                      55                      60

        Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
                65                      70                      75                      80

        Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                            85                      90                      95

        Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                    100                     105                     110

        Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
                    115                     120                     125

        Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
                    130                     135                     140
```

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
                180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
                195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
                210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
                260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
                275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                   325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                   340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
              355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
         370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                   405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

       435   440   445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

       450   455   460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

       465   470   475   480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

          485   490   495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

        500   505   510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

       515   520   525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

      530   535   540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545   550   555   560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565   570   575

Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
                580   585   590

Ser Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu His Phe Arg
                595   600   605

Trp Gly Ser Pro Pro Lys Asp
                610   615

<210> 36

<211> 630

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/asK21MSHa

<400> 36

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
  1   5   10   15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
          35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
       50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
     65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
          115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
     130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
             165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
             180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
             195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
           210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                 245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
             260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
             275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
             290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                    325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
                355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
            370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly
           580   585   590

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
           595   600   605

Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Tyr Ser Met Glu His Phe
           610   615   620

Arg Trp Gly Lys Pro Val
625   630

<210> 37

<211> 630

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/gsK21MSHa

<400> 37

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
    1   5   10   15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20   25   30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

  35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

 50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

 65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

   85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

   100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

   115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

   130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
                180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
                195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
                210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
                260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
                275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
                290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
                355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
                370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450   455   460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                 485   490   495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
             500   505   510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
             515   520   525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530   535   540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545   550   555   560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
             565   570   575

Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
        580   585   590

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
        595   600   605

Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Tyr Ser Met Glu His Phe
    610   615   620

Arg Trp Gly Lys Pro Val
625   630

<210> 38

<211> 640

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/asK21MSHb

<400> 38

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1   5   10   15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
        50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
    65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
        130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
            210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
            275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
            290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
         325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
         340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
         355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
         370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
         405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
         420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

                    435   440   445

    Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
           450   455   460

    Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
    465   470   475   480

    Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                            485   490   495

    Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
                   500   505   510

    Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
                515   520   525

    Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
           530   535   540

    Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
    545   550   555   560

    His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                   565   570   575

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Pro Gly
580   585   590

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
595   600   605

Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Ala Glu Lys Lys Asp Glu
610   615   620

Gly Pro Tyr Arg Met Glu His Phe Arg Trp Gly Ser Pro Pro Lys Asp
625   630   635   640

<210> 39
<211> 640
<212> PRT
<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/gsK21MSHb

<400> 39
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1   5   10   15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
        50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
    65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                    85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
        130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                    165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
                    180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
                195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
                210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                    245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
                260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
                275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
                290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
                355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
            370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435   440   445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
        450   455   460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                485   490   495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500   505   510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
        515   520   525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530   535   540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545   550   555   560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            565   570   575

Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
         580   585   590

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
         595   600   605

Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Ala Glu Lys Lys Asp Glu
    610   615   620

Gly Pro Tyr Arg Met Glu His Phe Arg Trp Gly Ser Pro Pro Lys Asp
625   630   635   640